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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Forschungszentrum Borstel
 (B) STREET: Parkallee 1-40
 (C) CITY: Borstel
 (D) State: Schleswig-Holstein
 (E) COUNTRY: Germany
 (F) POSTAL CODE: D 23845

(ii) TITLE OF INVENTION: Antisense-Oligonucleotides for treating proliferating cells

(iii) NUMBER OF SEQUENCES: 3

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENZ CHARACTERISTICS:

(A) LENGTH: 12493 base pairs
 (B) TYPE: Nucleotid
 (C) STRANDEDNESS: dopple strand
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNS

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 197..9964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTACCGGGCG GAGGTGAGCG CGGCGCCGGC TCCTCCTGCG GCGGACTTTG GGTGCGACTT 60
 GACGAGCGGT GGTTCGACAA GTGGCCTTGC GGGCCGGATC GTCCCAGTGG AAGAGTTGTA 120
 AATTGCTTC TGGCCTTCCC CTACGGATTA TACCTGGCCT TCCCCTACGG ATTATACTCA 180
 ACTTACTGTT TAGAAA ATG TGG CCC ACG AGA CGC CTG GTT ACT ATC AAA 229
 Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys
 1 5 10
 AGG AGC GGG GTC GAC GGT CCC CAC TTT CCC CTG AGC CTC AGC ACC TGC 277
 Arg Ser Gly Val Asp Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys
 15 20 25
 TTG TTT GGA AGG GGT ATT GAA TGT GAC ATC CGT ATC CAG CTT CCT GTT 325
 Leu Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val
 30 35 40
 GTG TCA AAA CAA CAT TGC AAA GTT GAA ATC CAT GAG CAG GAG GCA ATA 373
 Val Ser Lys Gln His Cys Lys Val Glu Ile His Glu Gln Glu Ala Ile
 45 50 55

SUB
A2

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	TTA	CAT	AAT	TTC	AGT	TCC	ACA	AAT	CCA	ACA	CAA	GTA	AAT	GGG	TCT	GTT	421
	Leu	His	Asn	Phe	Ser	Ser	Thr	Asn	Pro	Thr	Gln	Val	Asn	Gly	Ser	Val	
	60					65					70					75	
5	ATT	GAT	GAG	CCT	GTA	CGG	CTA	AAA	CAT	GGA	GAT	GTA	ATA	ACT	ATT	ATT	469
	Ile	Asp	Glu	Pro	Val	Arg	Leu	Lys	His	Gly	Asp	Val	Ile	Thr	Ile	Ile	
					80					85					90		
10	GAT	CGT	TCC	TTC	AGG	TAT	GAA	AAT	GAA	AGT	CTT	CAG	AAT	GGA	AGG	AAG	517
	Asp	Arg	Ser	Phe	Arg	Tyr	Glu	Asn	Glu	Ser	Leu	Gln	Asn	Gly	Arg	Lys	
				95					100					105			
15	TCA	ACT	GAA	TTT	CCA	AGA	AAA	ATA	CGT	GAA	CAG	GAG	CCA	GCA	CGT	CGT	565
	Ser	Thr	Glu	Phe	Pro	Arg	Lys	Ile	Arg	Glu	Gln	Glu	Pro	Ala	Arg	Arg	
			110					115					120				
20	GTC	TCA	AGA	TCT	AGC	TTC	TCT	TCT	GAC	CCT	GAT	GAG	AAA	GCT	CAA	GAT	613
	Val	Ser	Arg	Ser	Ser	Phe	Ser	Ser	Asp	Pro	Asp	Glu	Lys	Ala	Gln	Asp	
		125					130					135					
25	TCC	AAG	GCC	TAT	TCA	AAA	ATC	ACT	GAA	GGA	AAA	GTT	TCA	GGA	AAT	CCT	661
	Ser	Lys	Ala	Tyr	Ser	Lys	Ile	Thr	Glu	Gly	Lys	Val	Ser	Gly	Asn	Pro	
	140					145					150					155	
30	CAG	GTA	CAT	ATC	AAG	AAT	GTC	AAA	GAA	GAC	AGT	ACC	GCA	GAT	GAC	TCA	709
	Gln	Val	His	Ile	Lys	Asn	Val	Lys	Glu	Asp	Ser	Thr	Ala	Asp	Asp	Ser	
					160					165					170		
35	AAA	GAC	AGT	GTT	GCT	CAG	GGA	ACA	ACT	AAT	GTT	CAT	TCC	TCA	GAA	CAT	757
	Lys	Asp	Ser	Val	Ala	Gln	Gly	Thr	Thr	Asn	Val	His	Ser	Ser	Glu	His	
				175					180					185			
40	GCT	GGA	CGT	AAT	GGC	AGA	AAT	GCA	GCT	GAT	CCC	ATT	TCT	GGG	GAT	TTT	805
	Ala	Gly	Arg	Asn	Gly	Arg	Asn	Ala	Ala	Asp	Pro	Ile	Ser	Gly	Asp	Phe	
			190					195					200				
45	AAA	GAA	ATT	TCC	AGC	GTT	AAA	TTA	GTG	AGC	CGT	TAT	GGA	GAA	TTG	AAG	853
	Lys	Glu	Ile	Ser	Ser	Val	Lys	Leu	Val	Ser	Arg	Tyr	Gly	Glu	Leu	Lys	
		205					210					215					
50	TCT	GTT	CCC	ACT	ACA	CAA	TGT	CTT	GAC	AAT	AGC	AAA	AAA	AAT	GAA	TCT	901
	Ser	Val	Pro	Thr	Thr	Gln	Cys	Leu	Asp	Asn	Ser	Lys	Lys	Asn	Glu	Ser	
		220				225					230					235	
55	CCC	TTT	TGG	AAG	CTT	TAT	GAG	TCA	GTG	AAG	AAA	GAG	TTG	GAT	GTA	AAA	949
	Pro	Phe	Trp	Lys	Leu	Tyr	Glu	Ser	Val	Lys	Lys	Glu	Leu	Asp	Val	Lys	
					240					245					250		
60	TCA	CAA	AAA	GAA	AAT	GTC	CTA	CAG	TAT	TGT	AGA	AAA	TCT	GGA	TTA	CAA	997
	Ser	Gln	Lys	Glu	Asn	Val	Leu	Gln	Tyr	Cys	Arg	Lys	Ser	Gly	Leu	Gln	
				255					260					265			
65	ACT	GAT	TAC	GCA	ACA	GAG	AAA	GAA	AGT	GCT	GAT	GGT	TTA	CAG	GGG	GAG	1045
	Thr	Asp	Tyr	Ala	Thr	Glu	Lys	Glu	Ser	Ala	Asp	Gly	Leu	Gln	Gly	Glu	
			270					275					280				
70	ACC	CAA	CTG	TTG	GTC	TCG	CGT	AAG	TCA	AGA	CCA	AAA	TCT	GGT	GGG	AGC	1093
	Thr	Gln	Leu	Leu	Val	Ser	Arg	Lys	Ser	Arg	Pro	Lys	Ser	Gly	Gly	Ser	
		285					290					295					
75	GGC	CAC	GCT	GTG	GCA	GAG	CCT	GCT	TCA	CCT	GAA	CAA	GAG	CTT	GAC	CAG	1141
	Gly	His	Ala	Val	Ala	Glu	Pro	Ala	Ser	Pro	Glu	Gln	Glu	Leu	Asp	Gln	
	300					305					310					315	

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	CCT	CCC	TTA	AGA	CGG	CAG	TGT	ATT	AGA	GAA	AAT	GGA	AAC	GTA	GCA	AAA	2725
	Pro	Pro	Leu	Arg	Arg	Gln	Cys	Ile	Arg	Glu	Asn	Gly	Asn	Val	Ala	Lys	
			830					835					840				
5	ACG	CCC	AGG	AAC	ACC	TAC	AAA	ATG	ACT	TCT	CTG	GAG	ACA	AAA	ACT	TCA	2773
	Thr	Pro	Arg	Asn	Thr	Tyr	Lys	Met	Thr	Ser	Leu	Glu	Thr	Lys	Thr	Ser	
		845					850					855					
10	GAT	ACT	GAG	ACA	GAG	CCT	TCA	AAA	ACA	GTA	TCC	ACT	GTA	AAC	AGG	TCA	2821
	Asp	Thr	Glu	Thr	Glu	Pro	Ser	Lys	Thr	Val	Ser	Thr	Val	Asn	Arg	Ser	
	860					865					870					875	
15	GGA	AGG	TCT	ACA	GAG	TTC	AGG	AAT	ATA	CAG	AAG	CTA	CCT	GTG	GAA	AGT	2869
	Gly	Arg	Ser	Thr	Glu	Phe	Arg	Asn	Ile	Gln	Lys	Leu	Pro	Val	Glu	Ser	
					880					885						890	
20	AAG	AGT	GAA	GAA	ACA	AAT	ACA	GAA	ATT	GTT	GAG	TGC	ATC	CTA	AAA	AGA	2917
	Lys	Ser	Glu	Glu	Thr	Asn	Thr	Glu	Ile	Val	Glu	Cys	Ile	Leu	Lys	Arg	
				895					900					905			
25	GGT	CAG	AAG	GCA	ACA	CTA	CTA	CAA	CAA	AGG	AGA	GAA	GGA	GAG	ATG	AAG	2965
	Gly	Gln	Lys	Ala	Thr	Leu	Leu	Gln	Gln	Arg	Arg	Glu	Gly	Glu	Met	Lys	
			910					915					920				
30	GAA	ATA	GAA	AGA	CCT	TTT	GAG	ACA	TAT	AAG	GAA	AAT	ATT	GAA	TTA	AAA	3013
	Glu	Ile	Glu	Arg	Pro	Phe	Glu	Thr	Tyr	Lys	Glu	Asn	Ile	Glu	Leu	Lys	
		925					930					935					
35	GAA	AAC	GAT	GAA	AAG	ATG	AAA	GCA	ATG	AAG	AGA	TCA	AGA	ACT	TGG	GGG	3061
	Glu	Asn	Asp	Glu	Lys	Met	Lys	Ala	Met	Lys	Arg	Ser	Arg	Thr	Trp	Gly	
	940					945					950					955	
40	CAG	AAA	TGT	GCA	CCA	ATG	TCT	GAC	CTG	ACA	GAC	CTC	AAG	AGC	TTG	CCT	3109
	Gln	Lys	Cys	Ala	Pro	Met	Ser	Asp	Leu	Thr	Asp	Leu	Lys	Ser	Leu	Pro	
					960				965						970		
45	GAT	ACA	GAA	CTC	ATG	AAA	GAC	ACG	GCA	CGT	GGC	CAG	AAT	CTC	CTC	CAA	3157
	Asp	Thr	Glu	Leu	Met	Lys	Asp	Thr	Ala	Arg	Gly	Gln	Asn	Leu	Leu	Gln	
				975				980						985			
50	ACC	CAA	GAT	CAT	GCC	AAG	GCA	CCA	AAG	AGT	GAG	AAA	GGC	AAA	ATC	ACT	3205
	Thr	Gln	Asp	His	Ala	Lys	Ala	Pro	Lys	Ser	Glu	Lys	Gly	Lys	Ile	Thr	
			990					995					1000				
55	AAA	ATG	CCC	TGC	CAG	TCA	TTA	CAA	CCA	GAA	CCA	ATA	AAC	ACC	CCA	ACA	3253
	Lys	Met	Pro	Cys	Gln	Ser	Leu	Gln	Pro	Glu	Pro	Ile	Asn	Thr	Pro	Thr	
		1005					1010					1015					
60	CAC	ACA	AAA	CAA	CAG	TTG	AAG	GCA	TCC	CTG	GGG	AAA	GTA	GGT	GTG	AAA	3301
	His	Thr	Lys	Gln	Gln	Leu	Lys	Ala	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	
	1020					1025					1030					1035	
65	GAA	GAG	CTC	CTA	GCA	GTC	GGC	AAG	TTC	ACA	CGG	ACG	TCA	GGG	GAG	ACC	3349
	Glu	Glu	Leu	Leu	Ala	Val	Gly	Lys	Phe	Thr	Arg	Thr	Ser	Gly	Glu	Thr	
					1040					1045					1050		
70	ACG	CAC	ACG	CAC	AGA	GAG	CCA	GCA	GGA	GAT	GGC	AAG	AGC	ATC	AGA	ACG	3397
	Thr	His	Thr	His	Arg	Glu	Pro	Ala	Gly	Asp	Gly	Lys	Ser	Ile	Arg	Thr	
				1055				1060						1065			
75	TTT	AAG	GAG	TCT	CCA	AAG	CAG	ATC	CTG	GAC	CCA	GCA	GCC	CGT	GTA	ACT	3445
	Phe	Lys	Glu	Ser	Pro	Lys	Gln	Ile	Leu	Asp	Pro	Ala	Ala	Arg	Val	Thr	
			1070					1075					1080				

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	GGA	ATG	AAG	AAG	TGG	CCA	AGA	ACG	CCT	AAG	GAA	GAG	GCC	CAG	TCA	CTA	3493
	Gly	Met	Lys	Lys	Trp	Pro	Arg	Thr	Pro	Lys	Glu	Glu	Ala	Gln	Ser	Leu	
	1085						1090					1095					
5	GAA	GAC	CTG	GCT	GGC	TTC	AAA	GAG	CTC	TTC	CAG	ACA	CCA	GGT	CCC	TCT	3541
	Glu	Asp	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	Pro	Ser	
	1100					1105					1110					1115	
10	GAG	GAA	TCA	ATG	ACT	GAT	GAG	AAA	ACT	ACC	AAA	ATA	GCC	TGC	AAA	TCT	3589
	Glu	Glu	Ser	Met	Thr	Asp	Glu	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	
					1120					1125					1130		
15	CCA	CCA	CCA	GAA	TCA	GTG	GAC	ACT	CCA	ACA	AGC	ACA	AAG	CAA	TGG	CCT	3637
	Pro	Pro	Pro	Glu	Ser	Val	Asp	Thr	Pro	Thr	Ser	Thr	Lys	Gln	Trp	Pro	
				1135					1140					1145			
20	AAG	AGA	AGT	CTC	AGG	AAA	GCA	GAT	GTA	GAG	GAA	GAA	TTC	TTA	GCA	CTC	3685
	Lys	Arg	Ser	Leu	Arg	Lys	Ala	Asp	Val	Glu	Glu	Glu	Phe	Leu	Ala	Leu	
			1150					1155					1160				
25	AGG	AAA	CTA	ACA	CCA	TCA	GCA	GGG	AAA	GCC	ATG	CTT	ACG	CCC	AAA	CCA	3733
	Arg	Lys	Leu	Thr	Pro	Ser	Ala	Gly	Lys	Ala	Met	Leu	Thr	Pro	Lys	Pro	
		1165					1170					1175					
30	GCA	GGA	GGT	GAT	GAG	AAA	GAC	ATT	AAA	GCA	TTT	ATG	GGA	ACT	CCA	GTG	3781
	Ala	Gly	Gly	Asp	Glu	Lys	Asp	Ile	Lys	Ala	Phe	Met	Gly	Thr	Pro	Val	
	1180					1185					1190					1195	
35	CAG	AAA	CTG	GAC	CTG	GCA	GGA	ACT	TTA	CCT	GGC	AGC	AAA	AGA	CAG	CTA	3829
	Gln	Lys	Leu	Asp	Leu	Ala	Gly	Thr	Leu	Pro	Gly	Ser	Lys	Arg	Gln	Leu	
					1200					1205					1210		
40	CAG	ACT	CCT	AAG	GAA	AAG	GCC	CAG	GCT	CTA	GAA	GAC	CTG	GCT	GGC	TTT	3877
	Gln	Thr	Pro	Lys	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Asp	Leu	Ala	Gly	Phe	
				1215					1220					1225			
45	AAA	GAG	CTC	TTC	CAG	ACT	CCT	GGT	CAC	ACC	GAG	GAA	TTA	GTG	GCT	GCT	3925
	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	His	Thr	Glu	Glu	Leu	Val	Ala	Ala	
		1230						1235					1240				
50	GGT	AAA	ACC	ACT	AAA	ATA	CCC	TGC	GAC	TCT	CCA	CAG	TCA	GAC	CCA	GTG	3973
	Gly	Lys	Thr	Thr	Lys	Ile	Pro	Cys	Asp	Ser	Pro	Gln	Ser	Asp	Pro	Val	
		1245					1250					1255					
55	GAC	ACC	CCA	ACA	AGC	ACA	AAG	CAA	CGA	CCC	AAG	AGA	AGT	ATC	AGG	AAA	4021
	Asp	Thr	Pro	Thr	Ser	Thr	Lys	Gln	Arg	Pro	Lys	Arg	Ser	Ile	Arg	Lys	
	1260					1265					1270					1275	
60	GCA	GAT	GTA	GAG	GGA	GAA	CTC	TTA	GCG	TGC	AGG	AAT	CTA	ATG	CCA	TCA	4069
	Ala	Asp	Val	Glu	Gly	Glu	Leu	Leu	Ala	Cys	Arg	Asn	Leu	Met	Pro	Ser	
					1280					1285					1290		
65	GCA	GGC	AAA	GCC	ATG	CAC	ACG	CCT	AAA	CCA	TCA	GTA	GGT	GAA	GAG	AAA	4117
	Ala	Gly	Lys	Ala	Met	His	Thr	Pro	Lys	Pro	Ser	Val	Gly	Glu	Glu	Lys	
				1295					1300					1305			
70	GAC	ATC	ATC	ATA	TTT	GTG	GGA	ACT	CCA	GTG	CAG	AAA	CTG	GAC	CTG	ACA	4165
	Asp	Ile	Ile	Ile	Phe	Val	Gly	Thr	Pro	Val	Gln	Lys	Leu	Asp	Leu	Thr	
				1310				1315					1320				
75	GAG	AAC	TTA	ACC	GGC	AGC	AAG	AGA	CGG	CCA	CAA	ACT	CCT	AAG	GAA	GAG	4213
	Glu	Asn	Leu	Thr	Gly	Ser	Lys	Arg	Arg	Pro	Gln	Thr	Pro	Lys	Glu	Glu	
		1325					1330					1335					

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	GCC CAG GCT CTG GAA GAC CTG ACT GGC TTT AAA GAG CTC TTC CAG ACC	4261
	Ala Gln Ala Leu Glu Asp Leu Thr Gly Phe Lys Glu Leu Phe Gln Thr	
	1340 1345 1350 1355	
5	CCT GGT CAT ACT GAA GAA GCA GTG GCT GCT GGC AAA ACT ACT AAA ATG	4309
	Pro Gly His Thr Glu Glu Ala Val Ala Gly Lys Thr Thr Lys Met	
	1360 1365 1370	
10	CCC TGC GAA TCT TCT CCA CCA GAA TCA GCA GAC ACC CCA ACA AGC ACA	4357
	Pro Cys Glu Ser Ser Pro Pro Glu Ser Ala Asp Thr Pro Thr Ser Thr	
	1375 1380 1385	
15	AGA AGG CAG CCC AAG ACA CCT TTG GAG AAA AGG GAC GTA CAG AAG GAG	4405
	Arg Arg Gln Pro Lys Thr Pro Leu Glu Lys Arg Asp Val Gln Lys Glu	
	1390 1395 1400	
20	CTC TCA GCC CTG AAG AAG CTC ACA CAG ACA TCA GGG GAA ACC ACA CAC	4453
	Leu Ser Ala Leu Lys Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His	
	1405 1410 1415	
25	ACA GAT AAA GTA CCA GGA GGT GAG GAT AAA AGC ATC AAC GCG TTT AGG	4501
	Thr Asp Lys Val Pro Gly Gly Glu Asp Lys Ser Ile Asn Ala Phe Arg	
	1420 1425 1430 1435	
30	GAA ACT GCA AAA CAG AAA CTG GAC CCA GCA GCA AGT GTA ACT GGT AGC	4549
	Glu Thr Ala Lys Gln Lys Leu Asp Pro Ala Ala Ser Val Thr Gly Ser	
	1440 1445 1450	
35	AAG AGG CAC CCA AAA ACT AAG GAA AAG GCC CAA CCC CTA GAA GAC CTG	4597
	Lys Arg His Pro Lys Thr Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu	
	1455 1460 1465	
40	GCT GGC TGG AAA GAG CTC TTC CAG ACA CCA GTA TGC ACT GAC AAG CCC	4645
	Ala Gly Trp Lys Glu Leu Phe Gln Thr Pro Val Cys Thr Asp Lys Pro	
	1470 1475 1480	
45	ACG ACT CAC GAG AAA ACT ACC AAA ATA GCC TGC AGA TCA CAA CCA GAC	4693
	Thr Thr His Glu Lys Thr Thr Lys Ile Ala Cys Arg Ser Gln Pro Asp	
	1485 1490 1495	
50	CCA GTG GAC ACA CCA ACA AGC TCC AAG CCA CAG TCC AAG AGA AGT CTC	4741
	Pro Val Asp Thr Pro Thr Ser Ser Lys Pro Gln Ser Lys Arg Ser Leu	
	1500 1505 1510 1515	
55	AGG AAA GTG GAC GTA GAA GAA GAA TTC TTC GCA CTC AGG AAA CGA ACA	4789
	Arg Lys Val Asp Val Glu Glu Glu Phe Phe Ala Leu Arg Lys Arg Thr	
	1520 1525 1530	
60	CCA TCA GCA GGC AAA GCC ATG CAC ACA CCC AAA CCA GCA GTA AGT GGT	4837
	Pro Ser Ala Gly Lys Ala Met His Thr Pro Lys Pro Ala Val Ser Gly	
	1535 1540 1545	
65	GAG AAA AAC ATC TAC GCA TTT ATG GGA ACT CCA GTG CAG AAA CTG GAC	4885
	Glu Lys Asn Ile Tyr Ala Phe Met Gly Thr Pro Val Gln Lys Leu Asp	
	1550 1555 1560	
70	CTG ACA GAG AAC TTA ACT GGC AGC AAG AGA CGG CTA CAA ACT CCT AAG	4933
	Leu Thr Glu Asn Leu Thr Gly Ser Lys Arg Arg Leu Gln Thr Pro Lys	
	1565 1570 1575	
75	GAA AAG GCC CAG GCT CTA GAA GAC CTG GCT GGC TTT AAA GAG CTC TTC	4981
	Glu Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe	
	1580 1585 1590 1595	

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	CAG	ACA	CGA	GGT	CAC	ACT	GAG	GAA	TCA	ATG	ACT	AAC	GAT	AAA	ACT	GCC	5029
	Gln	Thr	Arg	Gly	His	Thr	Glu	Glu	Ser	Met	Thr	Asn	Asp	Lys	Thr	Ala	
					1600					1605						1610	
5	AAA	GTA	GCC	TGC	AAA	TCT	TCA	CAA	CCA	GAC	CTA	GAC	AAA	AAC	CCA	GCA	5077
	Lys	Val	Ala	Cys	Lys	Ser	Ser	Gln	Pro	Asp	Leu	Asp	Lys	Asn	Pro	Ala	
				1615					1620						1625		
10	AGC	TCC	AAG	CGA	CGG	CTC	AAG	ACA	TCC	CTG	GGG	AAA	GTG	GGC	GTG	AAA	5125
	Ser	Ser	Lys	Arg	Arg	Leu	Lys	Thr	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	
			1630					1635					1640				
15	GAA	GAG	CTC	CTA	GCA	GTT	GGC	AAG	CTC	ACA	CAG	ACA	TCA	GGA	GAG	ACT	5173
	Glu	Glu	Leu	Leu	Ala	Val	Gly	Lys	Leu	Thr	Gln	Thr	Ser	Gly	Glu	Thr	
		1645					1650					1655					
20	ACA	CAC	ACA	CAC	ACA	GAG	CCA	ACA	GGA	GAT	GGT	AAG	AGC	ATG	AAA	GCA	5221
	Thr	His	Thr	His	Thr	Glu	Pro	Thr	Gly	Asp	Gly	Lys	Ser	Met	Lys	Ala	
	1660					1665					1670					1675	
25	TTT	ATG	GAG	TCT	CCA	AAG	CAG	ATC	TTA	GAC	TCA	GCA	GCA	AGT	CTA	ACT	5269
	Phe	Met	Glu	Ser	Pro	Lys	Gln	Ile	Leu	Asp	Ser	Ala	Ala	Ser	Leu	Thr	
					1680					1685					1690		
30	GAA	GAC	CTG	GCC	GGC	TTC	ATC	GAG	CTC	TTC	CAG	ACA	CCA	AGT	CAC	ACT	5365
	Glu	Asp	Leu	Ala	Gly	Phe	Ile	Glu	Leu	Phe	Gln	Thr	Pro	Ser	His	Thr	
			1710					1715					1720				
35	AAG	GAA	TCA	ATG	ACT	AAT	GAA	AAA	ACT	ACC	AAA	GTA	TCC	TAC	AGA	GCT	5413
	Lys	Glu	Ser	Met	Thr	Asn	Glu	Lys	Thr	Thr	Lys	Val	Ser	Tyr	Arg	Ala	
		1725					1730					1735					
40	TCA	CAG	CCA	GAC	CTA	GTG	GAC	ACC	CCA	ACA	AGC	TCC	AAG	CCA	CAG	CCC	5461
	Ser	Gln	Pro	Asp	Leu	Val	Asp	Thr	Pro	Thr	Ser	Ser	Lys	Pro	Gln	Pro	
	1740				1745						1750					1755	
45	AAG	AGA	AGT	CTC	AGG	AAA	GCA	GAC	ACT	GAA	GAA	GAA	TTT	TTA	GCA	TTT	5509
	Lys	Arg	Ser	Leu	Arg	Lys	Ala	Asp	Thr	Glu	Glu	Glu	Phe	Leu	Ala	Phe	
				1760						1765					1770		
50	AGG	AAA	CAA	ACG	CCA	TCA	GCA	GGC	AAA	GCC	ATG	CAC	ACA	CCC	AAA	CCA	5557
	Arg	Lys	Gln	Thr	Pro	Ser	Ala	Gly	Lys	Ala	Met	His	Thr	Pro	Lys	Pro	
				1775				1780						1785			
55	GCA	GTA	GGT	GAA	GAG	AAA	GAC	ATC	AAC	ACG	TTT	TTG	GGA	ACT	CCA	GTG	5605
	Ala	Val	Gly	Glu	Glu	Lys	Asp	Ile	Asn	Thr	Phe	Leu	Gly	Thr	Pro	Val	
			1790					1795					1800				
60	CAG	AAA	CTG	GAC	CAG	CCA	GGA	AAT	TTA	CCT	GGC	AGC	AAT	AGA	CGG	CTA	5653
	Gln	Lys	Leu	Asp	Gln	Pro	Gly	Asn	Leu	Pro	Gly	Ser	Asn	Arg	Arg	Leu	
		1805					1810					1815					
65	CAA	ACT	CGT	AAG	GAA	AAG	GCC	CAG	GCT	CTA	GAA	GAA	CTG	ACT	GGC	TTC	5701
	Gln	Thr	Arg	Lys	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Glu	Leu	Thr	Gly	Phe	
	1820					1825					1830					1835	
70	AGA	GAG	CTT	TTC	CAG	ACA	CCA	TGC	ACT	GAT	AAC	CCC	ACA	GCT	GAT	GAG	5749
	Arg	Glu	Leu	Phe	Gln	Thr	Pro	Cys	Thr	Asp	Asn	Pro	Thr	Ala	Asp	Glu	
					1840					1845					1850		

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	AAA	ACT	ACC	AAA	AAA	ATA	CTC	TGC	AAA	TCT	CCG	CAA	TCA	GAC	CCA	GCG	5797
	Lys	Thr	Thr	Lys	Lys	Ile	Leu	Cys	Lys	Ser	Pro	Gln	Ser	Asp	Pro	Ala	
				1855					1860					1865			
5	GAC	ACC	CCA	ACA	AAC	ACA	AAG	CAA	CGG	CCC	AAG	AGA	AGC	CTC	AAG	AAA	5845
	Asp	Thr	Pro	Thr	Asn	Thr	Lys	Gln	Arg	Pro	Lys	Arg	Ser	Leu	Lys	Lys	
				1870				1875					1880				
10	GCA	GAC	GTA	GAG	GAA	GAA	TTT	TTA	GCA	TTC	AGG	AAA	CTA	ACA	CCA	TCA	5893
	Ala	Asp	Val	Glu	Glu	Glu	Phe	Leu	Ala	Phe	Arg	Lys	Leu	Thr	Pro	Ser	
		1885					1890					1895					
15	GCA	GGC	AAA	GCC	ATG	CAC	ACG	CCT	AAA	GCA	GCA	GTA	GGT	GAA	GAG	AAA	5941
	Ala	Gly	Lys	Ala	Met	His	Thr	Pro	Lys	Ala	Ala	Val	Gly	Glu	Glu	Lys	
	1900					1905						1910				1915	
20	GAC	ATC	AAC	ACA	TTT	GTG	GGG	ACT	CCA	GTG	GAG	AAA	CTG	GAC	CTG	CTA	5989
	Asp	Ile	Asn	Thr	Phe	Val	Gly	Thr	Pro	Val	Glu	Lys	Leu	Asp	Leu	Leu	
					1920					1925					1930		
25	GGA	AAT	TTA	CCT	GGC	AGC	AAG	AGA	CGG	CCA	CAA	ACT	CCT	AAA	GAA	AAG	6037
	Gly	Asn	Leu	Pro	Gly	Ser	Lys	Arg	Arg	Pro	Gln	Thr	Pro	Lys	Glu	Lys	
				1935				1940						1945			
30	GCC	AAG	GCT	CTA	GAA	GAT	CTG	GCT	GGC	TTC	AAA	GAG	CTC	TTC	CAG	ACA	6085
	Ala	Lys	Ala	Leu	Glu	Asp	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	
			1950				1955						1960				
35	CCA	GGT	CAC	ACT	GAG	GAA	TCA	ATG	ACC	GAT	GAC	AAA	ATC	ACA	GAA	GTA	6133
	Pro	Gly	His	Thr	Glu	Glu	Ser	Met	Thr	Asp	Asp	Lys	Ile	Thr	Glu	Val	
		1965					1970					1975					
40	TCC	TGC	AAA	TCT	CCA	CAA	CCA	GAC	CCA	GTC	AAA	ACC	CCA	ACA	AGC	TCC	6181
	Ser	Cys	Lys	Ser	Pro	Gln	Pro	Asp	Pro	Val	Lys	Thr	Pro	Thr	Ser	Ser	
	1980					1985					1990					1995	
45	AAG	CAA	CGA	CTC	AAG	ATA	TCC	TTG	GGG	AAA	GTA	GGT	GTG	AAA	GAA	GAG	6229
	Lys	Gln	Arg	Leu	Lys	Ile	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	Glu	
					2000					2005					2010		
50	GTC	CTA	CCA	GTC	GGC	AAG	CTC	ACA	CAG	ACG	TCA	GGG	AAG	ACC	ACA	CAG	6277
	Val	Leu	Pro	Val	Gly	Lys	Leu	Thr	Gln	Thr	Ser	Gly	Lys	Thr	Thr	Gln	
				2015					2020					2025			
55	ACA	CAC	AGA	GAG	ACA	GCA	GGA	GAT	GGA	AAG	AGC	ATC	AAA	GCG	TTT	AAG	6325
	Thr	His	Arg	Glu	Thr	Ala	Gly	Asp	Gly	Lys	Ser	Ile	Lys	Ala	Phe	Lys	
			2030				2035						2040				
60	GAA	TCT	GCA	AAG	CAG	ATG	CTG	GAC	CCA	GCA	AAC	TAT	GGA	ACT	GGG	ATG	6373
	Glu	Ser	Ala	Lys	Gln	Met	Leu	Asp	Pro	Ala	Asn	Tyr	Gly	Thr	Gly	Met	
		2045				2050						2055					
65	GAG	AGG	TGG	CCA	AGA	ACA	CCT	AAG	GAA	GAG	GCC	CAA	TCA	CTA	GAA	GAC	6421
	Glu	Arg	Trp	Pro	Arg	Thr	Pro	Lys	Glu	Glu	Ala	Gln	Ser	Leu	Glu	Asp	
	2060					2065					2070					2075	
70	CTG	GCC	GGC	TTC	AAA	GAG	CTC	TTC	CAG	ACA	CCA	GAC	CAC	ACT	GAG	GAA	6469
	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Asp	His	Thr	Glu	Glu	
					2080					2085					2090		
75	TCA	ACA	ACT	GAT	GAC	AAA	ACT	ACC	AAA	ATA	GCC	TGC	AAA	TCT	CCA	CCA	6517
	Ser	Thr	Thr	Asp	Asp	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	Pro	Pro	
				2095					2100					2105			

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	CCA	GAA	TCA	ATG	GAC	ACT	CCA	ACA	AGC	ACA	AGG	AGG	CGG	CCC	AAA	ACA	6565
	Pro	Glu	Ser	Met	Asp	Thr	Pro	Thr	Ser	Thr	Arg	Arg	Arg	Pro	Lys	Thr	
			2110					2115					2120				
5	CCT	TTG	GGG	AAA	AGG	GAT	ATA	GTG	GAA	GAG	CTC	TCA	GCC	CTG	AAG	CAG	6613
	Pro	Leu	Gly	Lys	Arg	Asp	Ile	Val	Glu	Glu	Leu	Ser	Ala	Leu	Lys	Gln	
		2125					2130					2135					
10	CTC	ACA	CAG	ACC	ACA	CAC	ACA	GAC	AAA	GTA	CCA	GGA	GAT	GAG	GAT	AAA	6661
	Leu	Thr	Gln	Thr	Thr	His	Thr	Asp	Lys	Val	Pro	Gly	Asp	Glu	Asp	Lys	
	2140					2145					2150					2155	
15	GGC	ATC	AAC	GTG	TTC	AGG	GAA	ACT	GCA	AAA	CAG	AAA	CTG	GAC	CCA	GCA	6709
	Gly	Ile	Asn	Val	Phe	Arg	Glu	Thr	Ala	Lys	Gln	Lys	Leu	Asp	Pro	Ala	
					2160					2165					2170		
20	GCA	AGT	GTA	ACT	GGT	AGC	AAG	AGG	CAG	CCA	AGA	ACT	CCT	AAG	GGA	AAA	6757
	Ala	Ser	Val	Thr	Gly	Ser	Lys	Arg	Gln	Pro	Arg	Thr	Pro	Lys	Gly	Lys	
				2175					2180					2185			
25	GCC	CAA	CCC	CTA	GAA	GAC	TTG	GCT	GGC	TTG	AAA	GAG	CTC	TTC	CAG	ACA	6805
	Ala	Gln	Pro	Leu	Glu	Asp	Leu	Ala	Gly	Leu	Lys	Glu	Leu	Phe	Gln	Thr	
			2190					2195					2200				
30	CCA	GTA	TGC	ACT	GAC	AAG	CCC	ACG	ACT	CAC	GAG	AAA	ACT	ACC	AAA	ATA	6853
	Pro	Val	Cys	Thr	Asp	Lys	Pro	Thr	Thr	His	Glu	Lys	Thr	Thr	Lys	Ile	
		2205					2210					2215					
35	GCC	TGC	AGA	TCT	CCA	CAA	CCA	GAC	CCA	GTG	GGT	ACC	CCA	ACA	ATC	TTC	6901
	Ala	Cys	Arg	Ser	Pro	Gln	Pro	Asp	Pro	Val	Gly	Thr	Pro	Thr	Ile	Phe	
	2220					2225				2230					2235		
40	AAG	CCA	CAG	TCC	AAG	AGA	AGT	CTC	AGG	AAA	GCA	GAC	GTA	GAG	GAA	GAA	6949
	Lys	Pro	Gln	Ser	Lys	Arg	Ser	Leu	Arg	Lys	Ala	Asp	Val	Glu	Glu	Glu	
					2240					2245					2250		
45	TCC	TTA	GCA	CTC	AGG	AAA	CGA	ACA	CCA	TCA	GTA	GGG	AAA	GCT	ATG	GAC	6997
	Ser	Leu	Ala	Leu	Arg	Lys	Arg	Thr	Pro	Ser	Val	Gly	Lys	Ala	Met	Asp	
				2255					2260					2265			
50	ACA	CCC	AAA	CCA	GCA	GGA	GGT	GAT	GAG	AAA	GAC	ATG	AAA	GCA	TTT	ATG	7045
	Thr	Pro	Lys	Pro	Ala	Gly	Gly	Asp	Glu	Lys	Asp	Met	Lys	Ala	Phe	Met	
			2270					2275					2280				
55	GGA	ACT	CCA	GTG	CAG	AAA	TTG	GAC	CTG	CCA	GGA	AAT	TTA	CCT	GGC	AGC	7093
	Gly	Thr	Pro	Val	Gln	Lys	Leu	Asp	Leu	Pro	Gly	Asn	Leu	Pro	Gly	Ser	
		2285					2290					2295					
60	AAA	AGA	TGG	CCA	CAA	ACT	CCT	AAG	GAA	AAG	GCC	CAG	GCT	CTA	GAA	GAC	7141
	Lys	Arg	Trp	Pro	Gln	Thr	Pro	Lys	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Asp	
	2300					2305					2310					2315	
65	CTG	GCT	GGC	TTC	AAA	GAG	CTC	TTC	CAG	ACA	CCA	GGC	ACT	GAC	AAG	CCC	7189
	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	Thr	Asp	Lys	Pro	
				2320					2325						2330		
70	ACG	ACT	GAT	GAG	AAA	ACT	ACC	AAA	ATA	GCC	TGC	AAA	TCT	CCA	CAA	CCA	7237
	Thr	Thr	Asp	Glu	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	Pro	Gln	Pro	
				2335					2340					2345			
75	GAC	CCA	GTG	GAC	ACC	CCA	GCA	AGC	ACA	AAG	CAA	CGG	CCC	AAG	AGA	AAC	7285
	Asp	Pro	Val	Asp	Thr	Pro	Ala	Ser	Thr	Lys	Gln	Arg	Pro	Lys	Arg	Asn	
			2350					2355					2360				

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	CTC	AGG	AAA	GCA	GAC	GTA	GAG	GAA	GAA	TTT	TTA	GCA	CTC	AGG	AAA	CGA	7333
	Leu	Arg	Lys	Ala	Asp	Val	Glu	Glu	Glu	Phe	Leu	Ala	Leu	Arg	Lys	Arg	
		2365					2370					2375					
5	ACA	CCA	TCA	GCA	GGC	AAA	GCC	ATG	GAC	ACC	CCA	AAA	CCA	GCA	GTA	AGT	7381
	Thr	Pro	Ser	Ala	Gly	Lys	Ala	Met	Asp	Thr	Pro	Lys	Pro	Ala	Val	Ser	
	2380					2385					2390					2395	
10	GAT	GAG	AAA	AAT	ATC	AAC	ACA	TTT	GTG	GAA	ACT	CCA	GTG	CAG	AAA	CTG	7429
	Asp	Glu	Lys	Asn	Ile	Asn	Thr	Phe	Val	Glu	Thr	Pro	Val	Gln	Lys	Leu	
					2400					2405					2410		
15	GAC	CTG	CTA	GGA	AAT	TTA	CCT	GGC	AGC	AAG	AGA	CAG	CCA	CAG	ACT	CCT	7477
	Asp	Leu	Leu	Gly	Asn	Leu	Pro	Gly	Ser	Lys	Arg	Gln	Pro	Gln	Thr	Pro	
				2415					2420					2425			
20	AAG	GAA	AAG	GCT	GAG	GCT	CTA	GAG	GAC	CTG	GTT	GGC	TTC	AAA	GAA	CTC	7525
	Lys	Glu	Lys	Ala	Glu	Ala	Leu	Glu	Asp	Leu	Val	Gly	Phe	Lys	Glu	Leu	
			2430					2435					2440				
25	TTC	CAG	ACA	CCA	GGT	CAC	ACT	GAG	GAA	TCA	ATG	ACT	GAT	GAC	AAA	ATC	7573
	Phe	Gln	Thr	Pro	Gly	His	Thr	Glu	Glu	Ser	Met	Thr	Asp	Asp	Lys	Ile	
		2445					2450					2455					
30	ACA	GAA	GTA	TCC	TGT	AAA	TCT	CCA	CAG	CCA	GAG	TCA	TTC	AAA	ACC	TCA	7621
	Thr	Glu	Val	Ser	Cys	Lys	Ser	Pro	Gln	Pro	Glu	Ser	Phe	Lys	Thr	Ser	
	2460					2465					2470					2475	
35	AGA	AGC	TCC	AAG	CAA	AGG	CTC	AAG	ATA	CCC	CTG	GTG	AAA	GTG	GAC	ATG	7669
	Arg	Ser	Ser	Lys	Gln	Arg	Leu	Lys	Ile	Pro	Leu	Val	Lys	Val	Asp	Met	
					2480					2485					2490		
40	AAA	GAA	GAG	CCC	CTA	GCA	GTC	AGC	AAG	CTC	ACA	CGG	ACA	TCA	GGG	GAG	7717
	Lys	Glu	Glu	Pro	Leu	Ala	Val	Ser	Lys	Leu	Thr	Arg	Thr	Ser	Gly	Glu	
				2495					2500					2505			
45	ACT	ACG	CAA	ACA	CAC	ACA	GAG	CCA	ACA	GGA	GAT	AGT	AAG	AGC	ATC	AAA	7765
	Thr	Thr	Gln	Thr	His	Thr	Glu	Pro	Thr	Gly	Asp	Ser	Lys	Ser	Ile	Lys	
			2510					2515					2520				
50	GCG	TTT	AAG	GAG	TCT	CCA	AAG	CAG	ATC	CTG	GAC	CCA	GCA	GCA	AGT	GTA	7813
	Ala	Phe	Lys	Glu	Ser	Pro	Lys	Gln	Ile	Leu	Asp	Pro	Ala	Ala	Ser	Val	
		2525					2530					2535					
55	ACT	GGT	AGC	AGG	AGG	CAG	CTG	AGA	ACT	CGT	AAG	GAA	AAG	GCC	CGT	GCT	7861
	Thr	Gly	Ser	Arg	Arg	Gln	Leu	Arg	Thr	Arg	Lys	Glu	Lys	Ala	Arg	Ala	
	2540					2545					2550					2555	
60	CTA	GAA	GAC	CTG	GTT	GAC	TTC	AAA	GAG	CTC	TTC	TCA	GCA	CCA	GGT	CAC	7909
	Leu	Glu	Asp	Leu	Val	Asp	Phe	Lys	Glu	Leu	Phe	Ser	Ala	Pro	Gly	His	
					2560					2565					2570		
65	ACT	GAA	GAG	TCA	ATG	ACT	ATT	GAC	AAA	AAC	ACA	AAA	ATT	CCC	TGC	AAA	7957
	Thr	Glu	Glu	Ser	Met	Thr	Ile	Asp	Lys	Asn	Thr	Lys	Ile	Pro	Cys	Lys	
				2575					2580					2585			
70	TCT	CCC	CCA	CCA	GAA	CTA	ACA	GAC	ACT	GCC	ACG	AGC	ACA	AAG	AGA	TGC	8005
	Ser	Pro	Pro	Pro	Glu	Leu	Thr	Asp	Thr	Ala	Thr	Ser	Thr	Lys	Arg	Cys	
			2590					2595					2600				
75	CCC	AAG	ACA	CGT	CCC	AGG	AAA	GAA	GTA	AAA	GAG	GAG	CTC	TCA	GCA	GTT	8053
	Pro	Lys	Thr	Arg	Pro	Arg	Lys	Glu	Val	Lys	Glu	Glu	Leu	Ser	Ala	Val	
		2605					2610					2615					

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	GAG AGG CTC ACG CAA ACA TCA GGG CAA AGC ACA CAC ACA CAC AAA GAA	8101
	Glu Arg Leu Thr Gln Thr Ser Gly Gln Ser Thr His Thr His Lys Glu	
	2620 2625 2630 2635	
5	CCA GCA AGC GGT GAT GAG GGC ATC AAA GTA TTG AAG CAA CGT GCA AAG	8149
	Pro Ala Ser Gly Asp Glu Gly Ile Lys Val Leu Lys Gln Arg Ala Lys	
	2640 2645 2650	
10	AAG AAA CCA AAC CCA GTA GAA GAG GAA CCC AGC AGG AGA AGG CCA AGA	8197
	Lys Lys Pro Asn Pro Val Glu Glu Glu Pro Ser Arg Arg Arg Pro Arg	
	2655 2660 2665	
15	GCA CCT AAG GAA AAG GCC CAA CCC CTG GAA GAC CTG GCC GGC TTC ACA	8245
	Ala Pro Lys Glu Lys Ala Gln Pro Leu Glu Asp Leu Ala Gly Phe Thr	
	2670 2675 2680	
20	GAG CTC TCT GAA ACA TCA GGT CAC ACT CAG GAA TCA CTG ACT GCT GGC	8293
	Glu Leu Ser Glu Thr Ser Gly His Thr Gln Glu Ser Leu Thr Ala Gly	
	2685 2690 2695	
25	AAA GCC ACT AAA ATA CCC TGC GAA TCT CCC CCA CTA GAA GTG GTA GAC	8341
	Lys Ala Thr Lys Ile Pro Cys Glu Ser Pro Pro Leu Glu Val Val Asp	
	2700 2705 2710 2715	
30	ACC ACA GCA AGC ACA AAG AGG CAT CTC AGG ACA CGT GTG CAG AAG GTA	8389
	Thr Thr Ala Ser Thr Lys Arg His Leu Arg Thr Arg Val Gln Lys Val	
	2720 2725 2730	
35	CAA GTA AAA GAA GAG CCT TCA GCA GTC AAG TTC ACA CAA ACA TCA GGG	8437
	Gln Val Lys Glu Glu Pro Ser Ala Val Lys Phe Thr Gln Thr Ser Gly	
	2735 2740 2745	
40	GAA ACC ACG GAT GCA GAC AAA GAA CCA GCA GGT GAA GAT AAA GGC ATC	8485
	Glu Thr Thr Asp Ala Asp Lys Glu Pro Ala Gly Glu Asp Lys Gly Ile	
	2750 2755 2760	
45	AAA GCA TTG AAG GAA TCT GCA AAA CAG ACA CCG GCT CCA GCA GCA AGT	8533
	Lys Ala Leu Lys Glu Ser Ala Lys Gln Thr Pro Ala Pro Ala Ala Ser	
	2765 2770 2775	
50	GTA ACT GGC AGC AGG AGA CGG CCA AGA GCA CCC AGG GAA AGT GCC CAA	8581
	Val Thr Gly Ser Arg Arg Arg Pro Arg Ala Pro Arg Glu Ser Ala Gln	
	2780 2785 2790 2795	
55	GCC ATA GAA GAC CTA GCT GGC TTC AAA GAC CCA GCA GCA GGT CAC ACT	8629
	Ala Ile Glu Asp Leu Ala Gly Phe Lys Asp Pro Ala Ala Gly His Thr	
	2800 2805 2810	
60	GAA GAA TCA ATG ACT GAT GAC AAA ACC ACT AAA ATA CCC TGC AAA TCA	8677
	Glu Glu Ser Met Thr Asp Asp Lys Thr Thr Lys Ile Pro Cys Lys Ser	
	2815 2820 2825	
65	TCA CCA GAA CTA GAA GAC ACC GCA ACA AGC TCA AAG AGA CGG CCC AGG	8725
	Ser Pro Glu Leu Glu Asp Thr Ala Thr Ser Ser Lys Arg Arg Pro Arg	
	2830 2835 2840	
70	ACA CGT GCC CAG AAA GTA GAA GTG AAG GAG GAG CTG TTA GCA GTT GGC	8773
	Thr Arg Ala Gln Lys Val Glu Val Lys Glu Glu Leu Leu Ala Val Gly	
	2845 2850 2855	
75	AAG CTC ACA CAA ACC TCA GGG GAG ACC ACG CAC ACC GAC AAA GAG CCG	8821
	Lys Leu Thr Gln Thr Ser Gly Glu Thr Thr His Thr Asp Lys Glu Pro	
	2860 2865 2870 2875	

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	GTA	GGT	GAG	GGC	AAA	GGC	ACG	AAA	GCA	TTT	AAG	CAA	CCT	GCA	AAG	CGG	8869
	Val	Gly	Glu	Gly	Lys	Gly	Thr	Lys	Ala	Phe	Lys	Gln	Pro	Ala	Lys	Arg	
					2880					2885					2890		
5	AAC	GTG	GAC	GCA	GAA	GAT	GTA	ATT	GGC	AGC	AGG	AGA	CAG	CCA	AGA	GCA	8917
	Asn	Val	Asp	Ala	Glu	Asp	Val	Ile	Gly	Ser	Arg	Arg	Gln	Pro	Arg	Ala	
				2895					2900					2905			
10	CCT	AAG	GAA	AAG	GCC	CAA	CCC	CTG	GAA	GAC	CTG	GCC	AGC	TTC	CAA	GAG	8965
	Pro	Lys	Glu	Lys	Ala	Gln	Pro	Leu	Glu	Asp	Leu	Ala	Ser	Phe	Gln	Glu	
			2910					2915					2920				
15	CTC	TCT	CAA	ACA	CCA	GGC	CAC	ACT	GAG	GAA	CTG	GCA	AAT	GGT	GCT	GCT	9013
	Leu	Ser	Gln	Thr	Pro	Gly	His	Thr	Glu	Glu	Leu	Ala	Asn	Gly	Ala	Ala	
		2925					2930					2935					
20	GAT	AGC	TTT	ACA	AGC	GCT	CCA	AAG	CAA	ACA	CCT	GAC	AGT	GGA	AAA	CCT	9061
	Asp	Ser	Phe	Thr	Ser	Ala	Pro	Lys	Gln	Thr	Pro	Asp	Ser	Gly	Lys	Pro	
	2940				2945						2950				2955		
25	CTA	AAA	ATA	TCC	AGA	AGA	GTT	CTT	CGG	GCC	CCT	AAA	GTA	GAA	CCC	GTG	9109
	Leu	Lys	Ile	Ser	Arg	Arg	Val	Leu	Arg	Ala	Pro	Lys	Val	Glu	Pro	Val	
					2960				2965						2970		
30	GGA	GAC	GTG	GTA	AGC	ACC	AGA	GAC	CCT	GTA	AAA	TCA	CAA	AGC	AAA	AGC	9157
	Gly	Asp	Val	Val	Ser	Thr	Arg	Asp	Pro	Val	Lys	Ser	Gln	Ser	Lys	Ser	
			2975						2980					2985			
35	AAC	ACT	TCC	CTG	CCC	CCA	CTG	CCC	TTC	AAG	AGG	GGA	GGT	GGC	AAA	GAT	9205
	Asn	Thr	Ser	Leu	Pro	Pro	Leu	Pro	Phe	Lys	Arg	Gly	Gly	Gly	Lys	Asp	
			2990				2995						3000				
40	GGA	AGC	GTC	ACG	GGA	ACC	AAG	AGG	CTG	CGC	TGC	ATG	CCA	GCA	CCA	GAG	9253
	Gly	Ser	Val	Thr	Gly	Thr	Lys	Arg	Leu	Arg	Cys	Met	Pro	Ala	Pro	Glu	
	3005						3010				3015						
45	GAA	ATT	GTG	GAG	GAG	CTG	CCA	GCC	AGC	AAG	AAG	CAG	AGG	GTT	GCT	CCC	9301
	Glu	Ile	Val	Glu	Glu	Leu	Pro	Ala	Ser	Lys	Lys	Gln	Arg	Val	Ala	Pro	
	3020					3025					3030					3035	
50	AGG	GCA	AGA	GGC	AAA	TCA	TCC	GAA	CCC	GTG	GTC	ATC	ATG	AAG	AGA	AGT	9349
	Arg	Ala	Arg	Gly	Lys	Ser	Ser	Glu	Pro	Val	Val	Ile	Met	Lys	Arg	Ser	
				3040					3045						3050		
55	TTG	AGG	ACT	TCT	GCA	AAA	AGA	ATT	GAA	CCT	GCG	GAA	GAG	CTG	AAC	AGC	9397
	Leu	Arg	Thr	Ser	Ala	Lys	Arg	Ile	Glu	Pro	Ala	Glu	Glu	Leu	Asn	Ser	
			3055						3060					3065			
60	AAC	GAC	ATG	AAA	ACC	AAC	AAA	GAG	GAA	CAC	AAA	TTA	CAA	GAC	TCG	GTC	9445
	Asn	Asp	Met	Lys	Thr	Asn	Lys	Glu	Glu	His	Lys	Leu	Gln	Asp	Ser	Val	
			3070				3075					3080					
65	CCT	GAA	AAT	AAG	GGA	ATA	TCC	CTG	CGC	TCC	AGA	CGC	CAA	GAT	AAG	ACT	9493
	Pro	Glu	Asn	Lys	Gly	Ile	Ser	Leu	Arg	Ser	Arg	Arg	Gln	Asp	Lys	Thr	
		3085					3090					3095					
70	GAG	GCA	GAA	CAG	CAA	ATA	ACT	GAG	GTC	TTT	GTA	TTA	GCA	GAA	AGA	ATA	9541
	Glu	Ala	Glu	Gln	Gln	Ile	Thr	Glu	Val	Phe	Val	Leu	Ala	Glu	Arg	Ile	
	3100					3105					3110					3115	
75	GAA	ATA	AAC	AGA	AAT	GAA	AAG	AAG	CCC	ATG	AAG	ACC	TCC	CCA	GAG	ATG	9589
	Glu	Ile	Asn	Arg	Asn	Glu	Lys	Lys	Pro	Met	Lys	Thr	Ser	Pro	Glu	Met	
				3120					3125						3130		

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	GAC ATT CAG AAT CCA GAT GAT GGA GCC CGG AAA CCC ATA CCT AGA GAC	9637
	Asp Ile Gln Asn Pro Asp Asp Gly Ala Arg Lys Pro Ile Pro Arg Asp	
	3135 3140 3145	
5	AAA GTC ACT GAG AAC AAA AGG TGC TTG AGG TCT GCT AGA CAG AAT GAG	9685
	Lys Val Thr Glu Asn Lys Arg Cys Leu Arg Ser Ala Arg Gln Asn Glu	
	3150 3155 3160	
10	AGC TCC CAG CCT AAG GTG GCA GAG GAG AGC GGA GGG CAG AAG AGT GCG	9733
	Ser Ser Gln Pro Lys Val Ala Glu Glu Ser Gly Gly Gln Lys Ser Ala	
	3165 3170 3175	
15	AAG GTT CTC ATG CAG AAT CAG AAA GGG AAA GGA GAA GCA GGA AAT TCA	9781
	Lys Val Leu Met Gln Asn Gln Lys Gly Lys Gly Glu Ala Gly Asn Ser	
	3180 3185 3190 3195	
20	GAC TCC ATG TGC CTG AGA TCA AGA AAG ACA AAA AGC CAG CCT GCA GCA	9829
	Asp Ser Met Cys Leu Arg Ser Arg Lys Thr Lys Ser Gln Pro Ala Ala	
	3200 3205 3210	
	AGC ACT TTG GAG AGC AAA TCT GTG CAG AGA GTA ACG CGG AGT GTC AAG	9877
	Ser Thr Leu Glu Ser Lys Ser Val Gln Arg Val Thr Arg Ser Val Lys	
	3215 3220 3225	
25	AGG TGT GCA GAA AAT CCA AAG AAG GCT GAG GAC AAT GTG TGT GTC AAG	9925
	Arg Cys Ala Glu Asn Pro Lys Lys Ala Glu Asp Asn Val Cys Val Lys	
	3230 3235 3240	
30	AAA ATA ACA ACC AGA AGT CAT AGG GAC AGT GAA GAT ATT TGACAGAAAA	9974
	Lys Ile Thr Thr Arg Ser His Arg Asp Ser Glu Asp Ile	
	3245 3250 3255	
	ATCGAACTGG GAAAAATATA ATAAAGTTAG TTTTGTGATA AGTTCTAGTG CAGTTTTTGT	10034
35	CATAAATTAC AAGTGAATTC TGTAAGTAAG GCTGTCAGTC TGCTTAAGGG AAGAAAACTT	10094
	TGGATTTGCT GGGTCTGAAT CGGCTTCATA AACTCCACTG GGAGCACTGC TGGGCTCCTG	10154
40	GACTGAGAAT AGTTGAACAC CGGGGGCTTT GTGAAGGAGT CTGGGCCAAG GTTTGCCCTC	10214
	AGCTTTGCAG AATGAAGCCT TGAGGTCTGT CACCACCCAC AGCCACCCTA CAGCAGCCTT	10274
	AACTGTGACA CTTGCCACAC TGTGTCGTCG TTTGTTTGCC TATGTTCTCC AGGGCACGGT	10334
45	GGCAGGAACA ACTATCCTCG TCTGTCCCAA CACTGAGCAG GCACTCGGTA AACACGAATG	10394
	AATGGATAAG CGCACGGATG AATGGAGCTT ACAAGATCTG TCTTTCCAAT GGCCGGGGGC	10454
50	ATTTGGTCCC CAAATTAAGG CTATTGGACA TCTGCACAGG ACAGTCCTAT TTTTGATGTC	10514
	CTTTCCTTTC TGAAAATAAA GTTTTGTGCT TTGGAGAATG ACTCGTGAGC ACATCTTTAG	10574
	GGACCAAGAG TGACTTTCTG TAAGGAGTGA CTCGTGGCTT GCCTTGGTCT CTTGGGAATA	10634
55	CTTTTCTAAC TAGGGTTGCT CTCACCTGAG ACATTCTCCA CCCGCGGAAT CTCAGGGTCC	10694
	CAGGCTGTGG GCCATCACGA CCTCAAACCTG GCTCCTAATC TCCAGCTTTC CTGTCAATTGA	10754
60	AAGCTTCGGA AGTTTACTGG CTCTGCTCCC GCCTGTTTTT TTTCTGACTC TATCTGGCAG	10814
	CCCGATGCCA CCCAGTACAG GAAGTGACAC CAGTACTCTG TAAAGCATCA TCATCCTTGG	10874
65	AGAGACTGAG CACTCAGCAC CTTCAGCCAC GATTTAGGA TCGCTTCCTT GTGAGCCGCT	10934

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GCCTCCGAAA TCTCCTTTGA AGCCCAGACA TCTTTCTCCA GCTTCAGACT TG TAGATATA 10994
 ACTCGTTTCAT CTTCAATTTAC TTTCCACTTT GCCCCCTGTC CTCTCTGTGT TCCCCAAATC 11054
 5 AGAGAATAGC CCGCCATCCC CCAGATCACC TGTCTGGATT CCTCCCCATT CACCCACCTT 11114
 GCCAGGTGCA GGTGAGGATG GTGCACCAGA CAGGGTAGCT GTCCCCCAA ATGTGCCCTG 11174
 10 TCGGGGCAGT GCCCTGTCTC CACGTTTGTT TCCCAGTGT CTGGCGGGGA GCCAGGTGAC 11234
 ATCATAAATA CTTGCTGAAT GAATGCAGAA ATCAGCGGTA CTGACTTGTA CTATATTGGC 11294
 TGCCATGATA GGGTTCTCAC AGCGTCATCC ATGATCGTAA GGGAGAATGA CATTCTGCTT 11354
 15 GAGGGAGGGA ATAGAAAGGG GCAGGGAGGG GACATCTGAG GGCTTCACAG GGCTGCAAAG 11414
 GGTACAGGGA TTGCACCAGG GCAGAACAGG GGAGGGTGTT CAAGGAAGAG TGGCTCTTAG 11474
 20 CAGAGGCACT TTGGAAGGTG TGAGGCATAA ATGCTTCCTT CTACGTAGGC CAACCTCAAA 11534
 ACTTTTCAGTA GGAATGTTGC TATGATCAAG TTGTTCTAAC ACTTTAGACT TAGTAGTAAT 11594
 TATGAACCTC ACATAGAAAA ATTCATCCA GCCATATGCC TGTGGAGTGG AATATTCTGT 11654
 25 TTAGTAGAAA AATCCTTTAG AGTTCAGCTC TAACCAGAAA TCTTGCTGAA GTATGTCAGC 11714
 ACCTTTTCTC ACCCTGGTAA GTACAGTATT TCAAGAGCAC GCTAAGGGTG GTTTTCATTT 11774
 30 TACAGGGCTG TTGATGATGG GTTAAAAATG TTCATTTAAG GGCTACCCCC GTGTTTAATA 11834
 GATGAACACC ACTTCTACAC AACCTCCTT GGTACTGGGG GAGGGAGAGA TCTGACAAAT 11894
 ACTGCCATT CCCCTAGGCT GACTGGATTT GAGAACAAAT ACCCACCCTAT TTCCACCATG 11954
 35 GTATGGTAAC TTCTCTGAGC TTCAGTTTCC AAGTGAATTT CCATGTAATA GGACATTCCC 12014
 ATTAAATACA AGCTGTTTTT ACTTTTTCGC CTCCCAGGGC CTGTGCGATC TGGTCCCCCA 12074
 40 GCCTCTCTTG GGCTTTCTTA CACTAACTCT GTACCTACCA TCTCCTGCCT CCCTTAGGCA 12134
 GGCACCTCCA ACCACCACAC ACTCCCTGCT GTTTTCCCTG CCTGGAACCT TCCCACCAGC 12194
 CCCACCAAGA TCATTTTCATC CAGTCCTGAG CTCAGCTTAA GGGAGGCTTC TTGCCTGTGG 12254
 45 GTTCCCTCAC CCCCATGCCT GTCCTCCAGG CTGGGGCAGG TTCTTAGTTT GCCTGGAATT 12314
 GTTCTGTACC TCTTTGTAGC ACGTAGTGTT GTGAAACTAA GCCACTAATT GAGTTTCTGG 12374
 50 CTCCCCTCCT GGGGTTGTAA GTTTTGTTCA TTCATGAGGG CCGACTGTAT TTCCTGGTTA 12434
 CTGTATCCCA GTGACCAGCC ACAGGAGATG TCCAATAAAG TATGTGATGA AATGGTCTT 12493

(2) INFORMATION FOR SEQ ID NO: 2:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3256 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

60

- (ii) MOLECULE TYPE: Protein
 (xi) SEQUENCE DISCRIPTION: SEQ ID NO: 2:

65

Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg Ser Gly Val Asp
 1 5 10 15

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	Gly	Pro	His	Phe	Pro	Leu	Ser	Leu	Ser	Thr	Cys	Leu	Phe	Gly	Arg	Gly
				20					25					30		
5	Ile	Glu	Cys	Asp	Ile	Arg	Ile	Gln	Leu	Pro	Val	Val	Ser	Lys	Gln	His
			35					40					45			
	Cys	Lys	Val	Glu	Ile	His	Glu	Gln	Glu	Ala	Ile	Leu	His	Asn	Phe	Ser
		50					55					60				
10	Ser	Thr	Asn	Pro	Thr	Gln	Val	Asn	Gly	Ser	Val	Ile	Asp	Glu	Pro	Val
	65					70					75				80	
	Arg	Leu	Lys	His	Gly	Asp	Val	Ile	Thr	Ile	Ile	Asp	Arg	Ser	Phe	Arg
15					85					90					95	
	Tyr	Glu	Asn	Glu	Ser	Leu	Gln	Asn	Gly	Arg	Lys	Ser	Thr	Glu	Phe	Pro
				100					105					110		
20	Arg	Lys	Ile	Arg	Glu	Gln	Glu	Pro	Ala	Arg	Arg	Val	Ser	Arg	Ser	Ser
			115					120					125			
	Phe	Ser	Ser	Asp	Pro	Asp	Glu	Lys	Ala	Gln	Asp	Ser	Lys	Ala	Tyr	Ser
		130					135					140				
25	Lys	Ile	Thr	Glu	Gly	Lys	Val	Ser	Gly	Asn	Pro	Gln	Val	His	Ile	Lys
	145					150					155					160
	Asn	Val	Lys	Glu	Asp	Ser	Thr	Ala	Asp	Asp	Ser	Lys	Asp	Ser	Val	Ala
30					165					170					175	
	Gln	Gly	Thr	Thr	Asn	Val	His	Ser	Ser	Glu	His	Ala	Gly	Arg	Asn	Gly
				180					185					190		
35	Arg	Asn	Ala	Ala	Asp	Pro	Ile	Ser	Gly	Asp	Phe	Lys	Glu	Ile	Ser	Ser
			195					200					205			
	Val	Lys	Leu	Val	Ser	Arg	Tyr	Gly	Glu	Leu	Lys	Ser	Val	Pro	Thr	Thr
		210					215					220				
40	Gln	Cys	Leu	Asp	Asn	Ser	Lys	Lys	Asn	Glu	Ser	Pro	Phe	Trp	Lys	Leu
	225					230					235					240
	Tyr	Glu	Ser	Val	Lys	Lys	Glu	Leu	Asp	Val	Lys	Ser	Gln	Lys	Glu	Asn
45					245					250					255	
	Val	Leu	Gln	Tyr	Cys	Arg	Lys	Ser	Gly	Leu	Gln	Thr	Asp	Tyr	Ala	Thr
				260					265					270		
50	Glu	Lys	Glu	Ser	Ala	Asp	Gly	Leu	Gln	Gly	Glu	Thr	Gln	Leu	Leu	Val
		275						280					285			
	Ser	Arg	Lys	Ser	Arg	Pro	Lys	Ser	Gly	Gly	Ser	Gly	His	Ala	Val	Ala
		290					295					300				
55	Glu	Pro	Ala	Ser	Pro	Glu	Gln	Glu	Leu	Asp	Gln	Asn	Lys	Gly	Lys	Gly
	305					310					315					320
	Arg	Asp	Val	Glu	Ser	Val	Gln	Thr	Pro	Ser	Lys	Ala	Val	Gly	Ala	Ser
					325					330					335	
60	Phe	Pro	Leu	Tyr	Glu	Pro	Ala	Lys	Met	Lys	Thr	Pro	Val	Gln	Tyr	Ser
				340					345					350		

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	Gln	Gln	Gln	Asn	Ser	Pro	Gln	Lys	His	Lys	Asn	Lys	Asp	Leu	Tyr	Thr	
			355					360					365				
5	Thr	Gly	Arg	Arg	Glu	Ser	Val	Asn	Leu	Gly	Lys	Ser	Glu	Gly	Phe	Lys	
		370					375					380					
	Ala	Gly	Asp	Lys	Thr	Leu	Thr	Pro	Arg	Lys	Leu	Ser	Thr	Arg	Asn	Arg	
	385					390					395					400	
10	Thr	Pro	Ala	Lys	Val	Glu	Asp	Ala	Ala	Asp	Ser	Ala	Thr	Lys	Pro	Glu	
					405					410					415		
	Asn	Leu	Ser	Ser	Lys	Thr	Arg	Gly	Ser	Ile	Pro	Thr	Asp	Val	Glu	Val	
				420					425					430			
15	Leu	Pro	Thr	Glu	Thr	Glu	Ile	His	Asn	Glu	Pro	Phe	Leu	Thr	Leu	Trp	
			435					440					445				
20	Leu	Thr	Gln	Val	Glu	Arg	Lys	Ile	Gln	Lys	Asp	Ser	Leu	Ser	Lys	Pro	
		450					455					460					
	Glu	Lys	Leu	Gly	Thr	Thr	Ala	Gly	Gln	Met	Cys	Ser	Gly	Leu	Pro	Gly	
	465					470					475					480	
25	Leu	Ser	Ser	Val	Asp	Ile	Asn	Asn	Phe	Gly	Asp	Ser	Ile	Asn	Glu	Ser	
					485					490					495		
	Glu	Gly	Ile	Pro	Leu	Lys	Arg	Arg	Arg	Val	Ser	Phe	Gly	Gly	His	Leu	
				500					505					510			
30	Arg	Pro	Glu	Leu	Phe	Asp	Glu	Asn	Leu	Pro	Pro	Asn	Thr	Pro	Leu	Lys	
			515					520					525				
35	Arg	Gly	Glu	Ala	Pro	Thr	Lys	Arg	Lys	Ser	Leu	Val	Met	His	Thr	Pro	
		530					535					540					
	Pro	Val	Leu	Lys	Lys	Ile	Ile	Lys	Glu	Gln	Pro	Gln	Pro	Ser	Gly	Lys	
	545					550					555					560	
40	Gln	Glu	Ser	Gly	Ser	Glu	Ile	His	Val	Glu	Val	Lys	Ala	Gln	Ser	Leu	
					565					570					575		
	Val	Ile	Ser	Pro	Pro	Ala	Pro	Ser	Pro	Arg	Lys	Thr	Pro	Val	Ala	Ser	
				580					585					590			
45	Asp	Gln	Arg	Arg	Arg	Ser	Cys	Lys	Thr	Ala	Pro	Ala	Ser	Ser	Ser	Lys	
			595					600					605				
	Ser	Gln	Thr	Glu	Val	Pro	Lys	Arg	Gly	Gly	Glu	Arg	Val	Ala	Thr	Cys	
		610					615					620					
	Leu	Gln	Lys	Arg	Val	Ser	Ile	Ser	Arg	Ser	Gln	His	Asp	Ile	Leu	Gln	
	625					630					635					640	
55	Met	Ile	Cys	Ser	Lys	Arg	Arg	Ser	Gly	Ala	Ser	Glu	Ala	Asn	Leu	Ile	
					645					650					655		
	Val	Ala	Lys	Ser	Trp	Ala	Asp	Val	Val	Lys	Leu	Gly	Ala	Lys	Gln	Thr	
				660					665					670			
60	Gln	Thr	Lys	Val	Ile	Lys	His	Gly	Pro	Gln	Arg	Ser	Met	Asn	Lys	Arg	
			675					680					685				
	Gln	Arg	Arg	Pro	Ala	Thr	Pro	Lys	Lys	Pro	Val	Gly	Glu	Val	His	Ser	
65		690					695					700					

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	Gln	Phe	Ser	Thr	Gly	His	Ala	Asn	Ser	Pro	Cys	Thr	Ile	Ile	Ile	Gly
	705					710					715					720
5	Lys	Ala	His	Thr	Glu	Lys	Val	His	Val	Pro	Ala	Arg	Pro	Tyr	Arg	Val
					725					730					735	
	Leu	Asn	Asn	Phe	Ile	Ser	Asn	Gln	Lys	Met	Asp	Phe	Lys	Glu	Asp	Leu
				740					745					750		
10	Ser	Gly	Ile	Ala	Glu	Met	Phe	Lys	Thr	Pro	Val	Lys	Glu	Gln	Pro	Gln
			755					760					765			
	Leu	Thr	Ser	Thr	Cys	His	Ile	Ala	Ile	Ser	Asn	Ser	Glu	Asn	Leu	Leu
		770					775					780				
15	Gly	Lys	Gln	Phe	Gln	Gly	Thr	Asp	Ser	Gly	Glu	Glu	Pro	Leu	Leu	Pro
	785					790					795					800
20	Thr	Ser	Glu	Ser	Phe	Gly	Gly	Asn	Val	Phe	Phe	Ser	Ala	Gln	Asn	Ala
					805					810					815	
	Ala	Lys	Gln	Pro	Ser	Asp	Lys	Cys	Ser	Ala	Ser	Pro	Pro	Leu	Arg	Arg
				820					825					830		
25	Gln	Cys	Ile	Arg	Glu	Asn	Gly	Asn	Val	Ala	Lys	Thr	Pro	Arg	Asn	Thr
			835					840					845			
	Tyr	Lys	Met	Thr	Ser	Leu	Glu	Thr	Lys	Thr	Ser	Asp	Thr	Glu	Thr	Glu
		850					855					860				
30	Pro	Ser	Lys	Thr	Val	Ser	Thr	Val	Asn	Arg	Ser	Gly	Arg	Ser	Thr	Glu
	865					870					875					880
	Phe	Arg	Asn	Ile	Gln	Lys	Leu	Pro	Val	Glu	Ser	Lys	Ser	Glu	Glu	Thr
35					885					890					895	
	Asn	Thr	Glu	Ile	Val	Glu	Cys	Ile	Leu	Lys	Arg	Gly	Gln	Lys	Ala	Thr
				900					905					910		
40	Leu	Leu	Gln	Gln	Arg	Arg	Glu	Gly	Glu	Met	Lys	Glu	Ile	Glu	Arg	Pro
			915					920					925			
	Phe	Glu	Thr	Tyr	Lys	Glu	Asn	Ile	Glu	Leu	Lys	Glu	Asn	Asp	Glu	Lys
		930					935					940				
45	Met	Lys	Ala	Met	Lys	Arg	Ser	Arg	Thr	Trp	Gly	Gln	Lys	Cys	Ala	Pro
	945					950					955					960
	Met	Ser	Asp	Leu	Thr	Asp	Leu	Lys	Ser	Leu	Pro	Asp	Thr	Glu	Leu	Met
50					965					970					975	
	Lys	Asp	Thr	Ala	Arg	Gly	Gln	Asn	Leu	Leu	Gln	Thr	Gln	Asp	His	Ala
				980					985					990		
55	Lys	Ala	Pro	Lys	Ser	Glu	Lys	Gly	Lys	Ile	Thr	Lys	Met	Pro	Cys	Gln
			995					1000					1005			
	Ser	Leu	Gln	Pro	Glu	Pro	Ile	Asn	Thr	Pro	Thr	His	Thr	Lys	Gln	Gln
		1010					1015					1020				
60	Leu	Lys	Ala	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	Glu	Leu	Leu	Ala
	1025					1030					1035					1040

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	Val Gly Lys Phe Thr Arg Thr Ser Gly Glu Thr Thr His Thr His Arg	1045	1050	1055
5	Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr Phe Lys Glu Ser Pro	1060	1065	1070
	Lys Gln Ile Leu Asp Pro Ala Ala Arg Val Thr Gly Met Lys Lys Trp	1075	1080	1085
10	Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu Glu Asp Leu Ala Gly	1090	1095	1100
	Phe Lys Glu Leu Phe Gln Thr Pro Gly Pro Ser Glu Glu Ser Met Thr	1105	1110	1115
15	Asp Glu Lys Thr Thr Lys Ile Ala Cys Lys Ser Pro Pro Pro Glu Ser	1125	1130	1135
20	Val Asp Thr Pro Thr Ser Thr Lys Gln Trp Pro Lys Arg Ser Leu Arg	1140	1145	1150
	Lys Ala Asp Val Glu Glu Glu Phe Leu Ala Leu Arg Lys Leu Thr Pro	1155	1160	1165
25	Ser Ala Gly Lys Ala Met Leu Thr Pro Lys Pro Ala Gly Gly Asp Glu	1170	1175	1180
	Lys Asp Ile Lys Ala Phe Met Gly Thr Pro Val Gln Lys Leu Asp Leu	1185	1190	1195
30	Ala Gly Thr Leu Pro Gly Ser Lys Arg Gln Leu Gln Thr Pro Lys Glu	1205	1210	1215
	Lys Ala Gln Ala Leu Glu Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln	1220	1225	1230
35	Thr Pro Gly His Thr Glu Glu Leu Val Ala Ala Gly Lys Thr Thr Lys	1235	1240	1245
40	Ile Pro Cys Asp Ser Pro Gln Ser Asp Pro Val Asp Thr Pro Thr Ser	1250	1255	1260
	Thr Lys Gln Arg Pro Lys Arg Ser Ile Arg Lys Ala Asp Val Glu Gly	1265	1270	1275
45	Glu Leu Leu Ala Cys Arg Asn Leu Met Pro Ser Ala Gly Lys Ala Met	1285	1290	1295
	His Thr Pro Lys Pro Ser Val Gly Glu Glu Lys Asp Ile Ile Ile Phe	1300	1305	1310
50	Val Gly Thr Pro Val Gln Lys Leu Asp Leu Thr Glu Asn Leu Thr Gly	1315	1320	1325
55	Ser Lys Arg Arg Pro Gln Thr Pro Lys Glu Glu Ala Gln Ala Leu Glu	1330	1335	1340
	Asp Leu Thr Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly His Thr Glu	1345	1350	1355
60	Glu Ala Val Ala Ala Gly Lys Thr Thr Lys Met Pro Cys Glu Ser Ser	1365	1370	1375
65	Pro Pro Glu Ser Ala Asp Thr Pro Thr Ser Thr Arg Arg Gln Pro Lys	1380	1385	1390

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	Thr	Pro	Leu	Glu	Lys	Arg	Asp	Val	Gln	Lys	Glu	Leu	Ser	Ala	Leu	Lys	
			1395					1400					1405				
5	Lys	Leu	Thr	Gln	Thr	Ser	Gly	Glu	Thr	Thr	His	Thr	Asp	Lys	Val	Pro	
		1410					1415					1420					
	Gly	Gly	Glu	Asp	Lys	Ser	Ile	Asn	Ala	Phe	Arg	Glu	Thr	Ala	Lys	Gln	
	1425					1430					1435					1440	
10	Lys	Leu	Asp	Pro	Ala	Ala	Ser	Val	Thr	Gly	Ser	Lys	Arg	His	Pro	Lys	
					1445					1450					1455		
	Thr	Lys	Glu	Lys	Ala	Gln	Pro	Leu	Glu	Asp	Leu	Ala	Gly	Trp	Lys	Glu	
15				1460					1465					1470			
	Leu	Phe	Gln	Thr	Pro	Val	Cys	Thr	Asp	Lys	Pro	Thr	Thr	His	Glu	Lys	
		1475						1480					1485				
20	Thr	Thr	Lys	Ile	Ala	Cys	Arg	Ser	Gln	Pro	Asp	Pro	Val	Asp	Thr	Pro	
	1490						1495					1500					
	Thr	Ser	Ser	Lys	Pro	Gln	Ser	Lys	Arg	Ser	Leu	Arg	Lys	Val	Asp	Val	
	1505					1510					1515					1520	
25	Glu	Glu	Glu	Phe	Phe	Ala	Leu	Arg	Lys	Arg	Thr	Pro	Ser	Ala	Gly	Lys	
				1525						1530					1535		
	Ala	Met	His	Thr	Pro	Lys	Pro	Ala	Val	Ser	Gly	Glu	Lys	Asn	Ile	Tyr	
30				1540					1545					1550			
	Ala	Phe	Met	Gly	Thr	Pro	Val	Gln	Lys	Leu	Asp	Leu	Thr	Glu	Asn	Leu	
		1555						1560					1565				
35	Thr	Gly	Ser	Lys	Arg	Arg	Leu	Gln	Thr	Pro	Lys	Glu	Lys	Ala	Gln	Ala	
	1570						1575					1580					
	Leu	Glu	Asp	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Arg	Gly	His	
	1585					1590					1595					1600	
40	Thr	Glu	Glu	Ser	Met	Thr	Asn	Asp	Lys	Thr	Ala	Lys	Val	Ala	Cys	Lys	
				1605						1610					1615		
	Ser	Ser	Gln	Pro	Asp	Leu	Asp	Lys	Asn	Pro	Ala	Ser	Ser	Lys	Arg	Arg	
45				1620					1625					1630			
	Leu	Lys	Thr	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	Glu	Leu	Leu	Ala	
		1635						1640					1645				
50	Val	Gly	Lys	Leu	Thr	Gln	Thr	Ser	Gly	Glu	Thr	Thr	His	Thr	His	Thr	
	1650					1655						1660					
	Glu	Pro	Thr	Gly	Asp	Gly	Lys	Ser	Met	Lys	Ala	Phe	Met	Glu	Ser	Pro	
	1665					1670					1675					1680	
55	Lys	Gln	Ile	Leu	Asp	Ser	Ala	Ala	Ser	Leu	Thr	Gly	Ser	Lys	Arg	Gln	
				1685						1690					1695		
	Leu	Arg	Thr	Pro	Lys	Gly	Lys	Ser	Glu	Val	Pro	Glu	Asp	Leu	Ala	Gly	
60				1700					1705					1710			
	Phe	Ile	Glu	Leu	Phe	Gln	Thr	Pro	Ser	His	Thr	Lys	Glu	Ser	Met	Thr	
		1715						1720					1725				

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	Asn	Glu	Lys	Thr	Thr	Lys	Val	Ser	Tyr	Arg	Ala	Ser	Gln	Pro	Asp	Leu	
	1730						1735					1740					
5	Val	Asp	Thr	Pro	Thr	Ser	Ser	Lys	Pro	Gln	Pro	Lys	Arg	Ser	Leu	Arg	
	1745					1750					1755					1760	
	Lys	Ala	Asp	Thr	Glu	Glu	Glu	Phe	Leu	Ala	Phe	Arg	Lys	Gln	Thr	Pro	
					1765					1770					1775		
10	Ser	Ala	Gly	Lys	Ala	Met	His	Thr	Pro	Lys	Pro	Ala	Val	Gly	Glu	Glu	
				1780					1785					1790			
	Lys	Asp	Ile	Asn	Thr	Phe	Leu	Gly	Thr	Pro	Val	Gln	Lys	Leu	Asp	Gln	
			1795					1800					1805				
15	Pro	Gly	Asn	Leu	Pro	Gly	Ser	Asn	Arg	Arg	Leu	Gln	Thr	Arg	Lys	Glu	
	1810						1815					1820					
20	Lys	Ala	Gln	Ala	Leu	Glu	Glu	Leu	Thr	Gly	Phe	Arg	Glu	Leu	Phe	Gln	
	1825					1830					1835					1840	
	Thr	Pro	Cys	Thr	Asp	Asn	Pro	Thr	Ala	Asp	Glu	Lys	Thr	Thr	Lys	Lys	
					1845					1850						1855	
25	Ile	Leu	Cys	Lys	Ser	Pro	Gln	Ser	Asp	Pro	Ala	Asp	Thr	Pro	Thr	Asn	
				1860					1865					1870			
	Thr	Lys	Gln	Arg	Pro	Lys	Arg	Ser	Leu	Lys	Lys	Ala	Asp	Val	Glu	Glu	
			1875					1880					1885				
30	Glu	Phe	Leu	Ala	Phe	Arg	Lys	Leu	Thr	Pro	Ser	Ala	Gly	Lys	Ala	Met	
	1890						1895					1900					
35	His	Thr	Pro	Lys	Ala	Ala	Val	Gly	Glu	Glu	Lys	Asp	Ile	Asn	Thr	Phe	
	1905				1910						1915					1920	
	Val	Gly	Thr	Pro	Val	Glu	Lys	Leu	Asp	Leu	Leu	Gly	Asn	Leu	Pro	Gly	
				1925						1930					1935		
40	Ser	Lys	Arg	Arg	Pro	Gln	Thr	Pro	Lys	Glu	Lys	Ala	Lys	Ala	Leu	Glu	
				1940					1945						1950		
	Asp	Leu	Ala	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	His	Thr	Glu	
		1955						1960					1965				
45	Glu	Ser	Met	Thr	Asp	Asp	Lys	Ile	Thr	Glu	Val	Ser	Cys	Lys	Ser	Pro	
	1970						1975					1980					
50	Gln	Pro	Asp	Pro	Val	Lys	Thr	Pro	Thr	Ser	Ser	Lys	Gln	Arg	Leu	Lys	
	1985					1990					1995					2000	
	Ile	Ser	Leu	Gly	Lys	Val	Gly	Val	Lys	Glu	Glu	Val	Leu	Pro	Val	Gly	
				2005						2010					2015		
55	Lys	Leu	Thr	Gln	Thr	Ser	Gly	Lys	Thr	Thr	Gln	Thr	His	Arg	Glu	Thr	
				2020					2025					2030			
	Ala	Gly	Asp	Gly	Lys	Ser	Ile	Lys	Ala	Phe	Lys	Glu	Ser	Ala	Lys	Gln	
		2035						2040					2045				
60	Met	Leu	Asp	Pro	Ala	Asn	Tyr	Gly	Thr	Gly	Met	Glu	Arg	Trp	Pro	Arg	
	2050						2055					2060					
65	Thr	Pro	Lys	Glu	Glu	Ala	Gln	Ser	Leu	Glu	Asp	Leu	Ala	Gly	Phe	Lys	
	2065					2070					2075					2080	

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	Glu	Leu	Phe	Gln	Thr	Pro	Asp	His	Thr	Glu	Glu	Ser	Thr	Thr	Asp	Asp	
						2085				2090					2095		
5	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	Pro	Pro	Pro	Glu	Ser	Met	Asp	
				2100					2105					2110			
	Thr	Pro	Thr	Ser	Thr	Arg	Arg	Arg	Pro	Lys	Thr	Pro	Leu	Gly	Lys	Arg	
			2115					2120					2125				
10	Asp	Ile	Val	Glu	Glu	Leu	Ser	Ala	Leu	Lys	Gln	Leu	Thr	Gln	Thr	Thr	
		2130					2135				2140						
	His	Thr	Asp	Lys	Val	Pro	Gly	Asp	Glu	Asp	Lys	Gly	Ile	Asn	Val	Phe	
15		2145				2150				2155						2160	
	Arg	Glu	Thr	Ala	Lys	Gln	Lys	Leu	Asp	Pro	Ala	Ala	Ser	Val	Thr	Gly	
				2165					2170						2175		
20	Ser	Lys	Arg	Gln	Pro	Arg	Thr	Pro	Lys	Gly	Lys	Ala	Gln	Pro	Leu	Glu	
				2180				2185					2190				
	Asp	Leu	Ala	Gly	Leu	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Val	Cys	Thr	Asp	
		2195					2200					2205					
25	Lys	Pro	Thr	Thr	His	Glu	Lys	Thr	Thr	Lys	Ile	Ala	Cys	Arg	Ser	Pro	
		2210				2215					2220						
	Gln	Pro	Asp	Pro	Val	Gly	Thr	Pro	Thr	Ile	Phe	Lys	Pro	Gln	Ser	Lys	
30		2225				2230				2235					2240		
	Arg	Ser	Leu	Arg	Lys	Ala	Asp	Val	Glu	Glu	Glu	Ser	Leu	Ala	Leu	Arg	
				2245					2250					2255			
35	Lys	Arg	Thr	Pro	Ser	Val	Gly	Lys	Ala	Met	Asp	Thr	Pro	Lys	Pro	Ala	
			2260				2265					2270					
	Gly	Gly	Asp	Glu	Lys	Asp	Met	Lys	Ala	Phe	Met	Gly	Thr	Pro	Val	Gln	
		2275				2280					2285						
40	Lys	Leu	Asp	Leu	Pro	Gly	Asn	Leu	Pro	Gly	Ser	Lys	Arg	Trp	Pro	Gln	
		2290				2295					2300						
	Thr	Pro	Lys	Glu	Lys	Ala	Gln	Ala	Leu	Glu	Asp	Leu	Ala	Gly	Phe	Lys	
45		2305			2310				2315				2320				
	Glu	Leu	Phe	Gln	Thr	Pro	Gly	Thr	Asp	Lys	Pro	Thr	Thr	Asp	Glu	Lys	
				2325				2330					2335				
50	Thr	Thr	Lys	Ile	Ala	Cys	Lys	Ser	Pro	Gln	Pro	Asp	Pro	Val	Asp	Thr	
			2340					2345					2350				
	Pro	Ala	Ser	Thr	Lys	Gln	Arg	Pro	Lys	Arg	Asn	Leu	Arg	Lys	Ala	Asp	
		2355				2360					2365						
55	Val	Glu	Glu	Glu	Phe	Leu	Ala	Leu	Arg	Lys	Arg	Thr	Pro	Ser	Ala	Gly	
		2370				2375				2380							
	Lys	Ala	Met	Asp	Thr	Pro	Lys	Pro	Ala	Val	Ser	Asp	Glu	Lys	Asn	Ile	
60		2385			2390			2395					2400				
	Asn	Thr	Phe	Val	Glu	Thr	Pro	Val	Gln	Lys	Leu	Asp	Leu	Leu	Gly	Asn	
				2405				2410					2415				

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	Leu	Pro	Gly	Ser	Lys	Arg	Gln	Pro	Gln	Thr	Pro	Lys	Glu	Lys	Ala	Glu	
					2420												2430
5	Ala	Leu	Glu	Asp	Leu	Val	Gly	Phe	Lys	Glu	Leu	Phe	Gln	Thr	Pro	Gly	
			2435					2440					2445				
	His	Thr	Glu	Glu	Ser	Met	Thr	Asp	Asp	Lys	Ile	Thr	Glu	Val	Ser	Cys	
		2450					2455					2460					
10	Lys	Ser	Pro	Gln	Pro	Glu	Ser	Phe	Lys	Thr	Ser	Arg	Ser	Ser	Lys	Gln	
	2465					2470					2475					2480	
	Arg	Leu	Lys	Ile	Pro	Leu	Val	Lys	Val	Asp	Met	Lys	Glu	Glu	Pro	Leu	
					2485					2490					2495		
15	Ala	Val	Ser	Lys	Leu	Thr	Arg	Thr	Ser	Gly	Glu	Thr	Thr	Gln	Thr	His	
				2500					2505					2510			
20	Thr	Glu	Pro	Thr	Gly	Asp	Ser	Lys	Ser	Ile	Lys	Ala	Phe	Lys	Glu	Ser	
		2515						2520					2525				
	Pro	Lys	Gln	Ile	Leu	Asp	Pro	Ala	Ala	Ser	Val	Thr	Gly	Ser	Arg	Arg	
		2530					2535					2540					
25	Gln	Leu	Arg	Thr	Arg	Lys	Glu	Lys	Ala	Arg	Ala	Leu	Glu	Asp	Leu	Val	
	2545					2550					2555					2560	
	Asp	Phe	Lys	Glu	Leu	Phe	Ser	Ala	Pro	Gly	His	Thr	Glu	Glu	Ser	Met	
					2565					2570					2575		
30	Thr	Ile	Asp	Lys	Asn	Thr	Lys	Ile	Pro	Cys	Lys	Ser	Pro	Pro	Pro	Glu	
				2580					2585					2590			
35	Leu	Thr	Asp	Thr	Ala	Thr	Ser	Thr	Lys	Arg	Cys	Pro	Lys	Thr	Arg	Pro	
		2595						2600					2605				
	Arg	Lys	Glu	Val	Lys	Glu	Glu	Leu	Ser	Ala	Val	Glu	Arg	Leu	Thr	Gln	
		2610					2615					2620					
40	Thr	Ser	Gly	Gln	Ser	Thr	His	Thr	His	Lys	Glu	Pro	Ala	Ser	Gly	Asp	
	2625					2630					2635					2640	
	Glu	Gly	Ile	Lys	Val	Leu	Lys	Gln	Arg	Ala	Lys	Lys	Lys	Pro	Asn	Pro	
					2645					2650					2655		
45	Val	Glu	Glu	Glu	Pro	Ser	Arg	Arg	Arg	Pro	Arg	Ala	Pro	Lys	Glu	Lys	
				2660					2665					2670			
50	Ala	Gln	Pro	Leu	Glu	Asp	Leu	Ala	Gly	Phe	Thr	Glu	Leu	Ser	Glu	Thr	
		2675						2680					2685				
	Ser	Gly	His	Thr	Gln	Glu	Ser	Leu	Thr	Ala	Gly	Lys	Ala	Thr	Lys	Ile	
		2690					2695					2700					
55	Pro	Cys	Glu	Ser	Pro	Pro	Leu	Glu	Val	Val	Asp	Thr	Thr	Ala	Ser	Thr	
	2705					2710					2715					2720	
	Lys	Arg	His	Leu	Arg	Thr	Arg	Val	Gln	Lys	Val	Gln	Val	Lys	Glu	Glu	

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Ser Ala Lys Gln Thr Pro Ala Pro Ala Ala Ser Val Thr Gly Ser Arg
 2770 2775 2780
 5 Arg Arg Pro Arg Ala Pro Arg Glu Ser Ala Gln Ala Ile Glu Asp Leu
 2785 2790 2795 2800
 Ala Gly Phe Lys Asp Pro Ala Ala Gly His Thr Glu Glu Ser Met Thr
 2805 2810 2815
 10 Asp Asp Lys Thr Thr Lys Ile Pro Cys Lys Ser Ser Pro Glu Leu Glu
 2820 2825 2830
 Asp Thr Ala Thr Ser Ser Lys Arg Arg Pro Arg Thr Arg Ala Gln Lys
 2835 2840 2845
 15 Val Glu Val Lys Glu Glu Leu Leu Ala Val Gly Lys Leu Thr Gln Thr
 2850 2855 2860
 Ser Gly Glu Thr Thr His Thr Asp Lys Glu Pro Val Gly Glu Gly Lys
 2865 2870 2875 2880
 Gly Thr Lys Ala Phe Lys Gln Pro Ala Lys Arg Asn Val Asp Ala Glu
 2885 2890 2895
 25 Asp Val Ile Gly Ser Arg Arg Gln Pro Arg Ala Pro Lys Glu Lys Ala
 2900 2905 2910
 Gln Pro Leu Glu Asp Leu Ala Ser Phe Gln Glu Leu Ser Gln Thr Pro
 2915 2920 2925
 30 Gly His Thr Glu Glu Leu Ala Asn Gly Ala Ala Asp Ser Phe Thr Ser
 2930 2935 2940
 Ala Pro Lys Gln Thr Pro Asp Ser Gly Lys Pro Leu Lys Ile Ser Arg
 2945 2950 2955 2960
 Arg Val Leu Arg Ala Pro Lys Val Glu Pro Val Gly Asp Val Val Ser
 2965 2970 2975
 40 Thr Arg Asp Pro Val Lys Ser Gln Ser Lys Ser Asn Thr Ser Leu Pro
 2980 2985 2990
 Pro Leu Pro Phe Lys Arg Gly Gly Gly Lys Asp Gly Ser Val Thr Gly
 2995 3000 3005
 45 Thr Lys Arg Leu Arg Cys Met Pro Ala Pro Glu Glu Ile Val Glu Glu
 3010 3015 3020
 Leu Pro Ala Ser Lys Lys Gln Arg Val Ala Pro Arg Ala Arg Gly Lys
 3025 3030 3035 3040
 Ser Ser Glu Pro Val Val Ile Met Lys Arg Ser Leu Arg Thr Ser Ala
 3045 3050 3055
 55 Lys Arg Ile Glu Pro Ala Glu Glu Leu Asn Ser Asn Asp Met Lys Thr
 3060 3065 3070
 Asn Lys Glu Glu His Lys Leu Gln Asp Ser Val Pro Glu Asn Lys Gly
 3075 3080 3085
 60 Ile Ser Leu Arg Ser Arg Arg Gln Asp Lys Thr Glu Ala Glu Gln Gln
 3090 3095 3100

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Ile Thr Glu Val Phe Val Leu Ala Glu Arg Ile Glu Ile Asn Arg Asn
3105 3110 3115 3120

Glu Lys Lys Pro Met Lys Thr Ser Pro Glu Met Asp Ile Gln Asn Pro
3125 3130 3135

Asp Asp Gly Ala Arg Lys Pro Ile Pro Arg Asp Lys Val Thr Glu Asn
3140 3145 3150

10 Lys Arg Cys Leu Arg Ser Ala Arg Gln Asn Glu Ser Ser Gln Pro Lys
3155 3160 3165

Val Ala Glu Glu Ser Gly Gly Gln Lys Ser Ala Lys Val Leu Met Gln
3170 3175 3180

15 Asn Gln Lys Gly Lys Gly Glu Ala Gly Asn Ser Asp Ser Met Cys Leu
3185 3190 3195 3200

20 Arg Ser Arg Lys Thr Lys Ser Gln Pro Ala Ala Ser Thr Leu Glu Ser
3205 3210 3215

Lys Ser Val Gln Arg Val Thr Arg Ser Val Lys Arg Cys Ala Glu Asn
3220 3225 3230

25 Pro Lys Lys Ala Glu Asp Asn Val Cys Val Lys Lys Ile Thr Thr Arg
3235 3240 3245

Ser His Arg Asp Ser Glu Asp Ile
3250 3255

30 (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 23 base pairs
35 (B) TYPE: Nucleotid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
40 (A) description: /desc = "synthetic oligonucleotide"

45 (xi) SEQUENCE DISCRIPTION: SEQ ID NO: 3:

ACCAGGCGTC TCGTGGGCCA CAT

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